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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/991,053

DATE: 06/06/2002
TIME: 14:54:39

Input Set : A:\Cu40CON1.APP
Output Set: N:\CRF3\06062002\I991053.raw

26

44->

ENTERED

3 <110> APPLICANT: Shimkets, Richard A.
5 <120> TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
6 MEGF-, AND ROUNDABOUT-LIKE POLYPEPTIDES
8 <130> FILE REFERENCE: 15966-540 CON S-10
10 <140> CURRENT APPLICATION NUMBER: 09/991,053
11 <141> CURRENT FILING DATE: 2002-05-23
13 <150> PRIOR APPLICATION NUMBER: USSN 60/123,667
14 <151> PRIOR FILING DATE: 1999-03-09
16 <150> PRIOR APPLICATION NUMBER: 09/520,781
17 <151> PRIOR FILING DATE: 2000-03-08
19 <160> NUMBER OF SEQ ID NOS: 81
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1812
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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29 <221> NAME/KEY: CDS
30 <222> LOCATION: (537)..(1535)
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35 ttttggttatt atgagtgtgc ttgcttatat aaaagaatat gcttaaggga aaaaagggtgc 120
37 tttaaagtta atattctaca aaccatagtt tatgagcata agaaattaca taatttacag 180
39 caatctgatg tattagtaat aataatgtat tattatctct taaacagtgt tttgttttat 240
41 ggctaacagt agcacctgtg aatgaggcag aacctgttat ttggatttca caaggatgtg 300
43 aaagtaatgg tactgttaaa agtaccacaaa atgtattata tgctttaaaa attctagcca 360
45 gaaaacagta ttttcctttt caacacatct attgaaagtg ttggataaat gcaggatgtt 420
47 aatatgctat aaacataaag tctgttttta aaaaatagca tttgaaaatc atgaagggtc 480
49 ttttggttttc ttttggtttgt atatatgttt attggtaaaa ggtgacactg gaagca atg 539
50 Met
51 1
53 aac acc aca gtg atg caa ggc ttc aac aga tct gag cgg tgc ccc aga 587
54 Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro Arg
55 5 10 15
57 gac act cgg ata gta cag ctg gta ttc cca gcc ctc tac aca gtg gtt 635
58 Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val Val
59 20 25 30
61 ttc ttg acc ggc atc ctg ctg aat act ttg gct ctg tgg gtg ttt gtt 683
62 Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe Val
63 35 40 45
65 cac atc ccc agc tcc tcc acc ttc atc atc tac ctc aaa aac act ttg 731
66 His Ile Pro Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr Leu
67 50 55 60 65

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69 gtg gcc gac ttg ata atg aca ctc atg ctt cct ttc aaa atc ctc tct 779
70 Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu Ser
71          70          75          80
73 gac tca cac ctg gca ccc tgg cag ctc aga gct ttt gtg tgt cgt ttt 827
74 Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg Phe
75          85          90          95
77 tct tcg gtg ata ttt tat gag acc atg tat gtg ggc atc gtg ctg tta 875
78 Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu Leu
79          100          105          110
81 ggg ctc ata gcc ttt gac aga ttc ctc aag atc atc aga cct ttg aga 923
82 Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu Arg
83          115          120          125
85 aat att ttt cta aaa aaa cct gtt ttt gca aaa acg gtc tca atc ttc 971
86 Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile Phe
87 130          135          140          145
89 atc tgg ttc ttt ttg ttc ttc atc tcc ctg cca aat atg atc ttg agc 1019
90 Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Met Ile Leu Ser
91          150          155          160
93 aac aag gaa gca aca cca tcg tct gtg aaa aag tgt gct tcc tta aag 1067
94 Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu Lys
95          165          170          175
97 ggg cct ctg ggg ctg aaa tgg cat caa atg gta aat aac ata tgc cag 1115
98 Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys Gln
99          180          185          190
101 ttt att ttc tgg act gtt ttt atc cta atg ctt gtg ttt tat gtg gtt 1163
102 Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val Val
103          195          200          205
105 att gca aaa aaa gta tat gat tct tat aga aag tcc aaa agt aag gac 1211
106 Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys Asp
107 210          215          220          225
109 aga aaa aac aac aaa aag ctg gaa ggc aaa gta ttt gtt gtc gtg gct 1259
110 Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val Ala
111          230          235          240
113 gtc ttc ttt gtg tgt ttt gct cca ttt cat ttt gcc aga gtt cca tat 1307
114 Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro Tyr
115          245          250          255
117 act cac agt caa acc aac aat aag act gac tgt aga ctg caa aat caa 1355
118 Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn Gln
119          260          265          270
121 ctg ttt att gct aaa gaa aca act ctc ttt ttg gca gca act aac att 1403
122 Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn Ile
123          275          280          285
125 tgt atg gat ccc tta ata tac ata ttc tta tgt aaa aaa ttc aca gaa 1451
126 Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr Glu
127 290          295          300          305
129 aag cta cca tgt atg caa ggg aga aag acc aca gca tca agc caa gaa 1499
130 Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln Glu
131          310          315          320
133 aat cat agc agt cag aca gac aac ata acc tta ggc tgacaactgt 1545

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134 Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly
135          325          330
137 acataggggtt aacttctatt tattgatgag acttccgtag ataatgtgga aatcaaattt 1605
139 aaccaagaaa aaaagatttg aacaaatgct ctcttacatt ttattatcct cgtgtacaga 1665
141 aaagattata taaaatttaa atccacatag atctattcat aagctgaatg aaccattact 1725
143 aagagaatgc aacaggatac aaatggccac tagaggtcat tatttctttc tttctttatt 1785
145 cagcgccgcg tttttttttt tttttttt 1812
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149 <211> LENGTH: 333
150 <212> TYPE: PRT
151 <213> ORGANISM: Homo sapiens
153 <400> SEQUENCE: 2
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155   1          5          10          15
157 Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val
158          20          25          30
160 Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe
161          35          40          45
163 Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr
164          50          55          60
166 Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu
167   65          70          75          80
169 Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg
170          85          90          95
172 Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu
173          100         105         110
175 Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu
176          115         120         125
178 Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile
179          130         135         140
181 Phe Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Met Ile Leu
182 145          150          155          160
184 Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu
185          165          170          175
187 Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys
188          180          185          190
190 Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val
191          195          200          205
193 Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys
194          210          215          220
196 Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val
197 225          230          235          240
199 Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro
200          245          250          255
202 Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn
203          260          265          270
205 Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn
206          275          280          285
208 Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr

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209      290      295      300
211 Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln
212 305      310      315      320
214 Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly
215      325      330
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220 <211> LENGTH: 3498
221 <212> TYPE: DNA
222 <213> ORGANISM: Homo sapiens
224 <220> FEATURE:
225 <221> NAME/KEY: CDS
226 <222> LOCATION: (214)..(3030)
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229 <221> NAME/KEY: misc_feature
230 <222> LOCATION: (3047)
231 <223> OTHER INFORMATION: an n may be any one of a or t or g or c
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236 gagagcgag cccgcggccc ggagagatcc cctcgataat ggattactaa atgggataca 120
238 cgctgtacca gttcgctccg agccccggcc gcctgtccgt cgatgcaccg aaaaggggtga 180
240 agtagagaaa taaagtctcc ccgctgaact act atg agg tca gaa gcc ttg ctg 234
241      Met Arg Ser Glu Ala Leu Leu
242      1      5
244 cta tat ttc aca ctg cta cac ttt gct ggg gct ggt ttc cca gaa gat 282
245 Leu Tyr Phe Thr Leu Leu His Phe Ala Gly Ala Gly Phe Pro Glu Asp
246      10      15      20
248 tct gag cca atc agt att tgc cat ggc aac tat aca aaa cag tat ccg 330
249 Ser Glu Pro Ile Ser Ile Ser His Gly Asn Tyr Thr Lys Gln Tyr Pro
250      25      30      35
252 gtg ttt gtg ggc cac aag cca gga cgg aac acc aca cag agg cac agg 378
253 Val Phe Val Gly His Lys Pro Gly Arg Asn Thr Thr Gln Arg His Arg
254 40      45      50      55
256 ctg gac atc cag atg att atg atc atg aac gga acc ctc tac att gct 426
257 Leu Asp Ile Gln Met Ile Met Ile Met Asn Gly Thr Leu Tyr Ile Ala
258      60      65      70
260 gct agg gac cat att tat act gtt gat ata gac aca tca cac acg gaa 474
261 Ala Arg Asp His Ile Tyr Thr Val Asp Ile Asp Thr Ser His Thr Glu
262      75      80      85
264 gaa att tat tgt agc aaa aaa ctg aca tgg aaa tct aga cag gcc gat 522
265 Glu Ile Tyr Cys Ser Lys Lys Leu Thr Trp Lys Ser Arg Gln Ala Asp
266      90      95      100
268 gta gac aca tgc aga atg aag gga aaa cat aag gat gag tgc cac aac 570
269 Val Asp Thr Cys Arg Met Lys Gly Lys His Lys Asp Glu Cys His Asn
270      105      110      115
272 ttt att aaa gtt ctt cta aag aaa aac gat gat gca ttg ttt gtc tgt 618
273 Phe Ile Lys Val Leu Leu Lys Lys Asn Asp Asp Ala Leu Phe Val Cys
274 120      125      130      135
276 gga act aat gcc ttc aac cct tcc tgc aga aac tat aag atg gat aca 666
277 Gly Thr Asn Ala Phe Asn Pro Ser Cys Arg Asn Tyr Lys Met Asp Thr

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278		140		145		150		
280	ttg gaa cca ttc ggg gat gaa ttc agc gga atg gcc aga tgc cca tat	714						
281	Leu Glu Pro Phe Gly Asp Glu Phe Ser Gly Met Ala Arg Cys Pro Tyr							
282		155		160		165		
284	gat gcc aaa cat gcc aac gtt gca ctg ttt gca gat gga aaa cta tac	762						
285	Asp Ala Lys His Ala Asn Val Ala Leu Phe Ala Asp Gly Lys Leu Tyr							
286		170		175		180		
288	tca gcc aca gtg act gac ttc ctt gcc att gac gca gtc att tac cgg	810						
289	Ser Ala Thr Val Thr Asp Phe Leu Ala Ile Asp Ala Val Ile Tyr Arg							
290		185		190		195		
292	agt ctt gga gaa agc cct acc ctg cgg acc gtc aag cac gat tca aaa	858						
293	Ser Leu Gly Glu Ser Pro Thr Leu Arg Thr Val Lys His Asp Ser Lys							
294	200		205		210		215	
296	tgg ttg aaa gaa cca tac ttt gtt caa gcc gtg gat tac gga gat tat	906						
297	Trp Leu Lys Glu Pro Tyr Phe Val Gln Ala Val Asp Tyr Gly Asp Tyr							
298		220		225		230		
300	atc tac ttc ttc ttc agg gaa ata gca gtg gag tat aac acc atg gga	954						
301	Ile Tyr Phe Phe Phe Arg Glu Ile Ala Val Glu Tyr Asn Thr Met Gly							
302		235		240		245		
304	aag gta gtt ttc cca aga gtg gct cag gtt tgt aag aat gat atg gga	1002						
305	Lys Val Val Phe Pro Arg Val Ala Gln Val Cys Lys Asn Asp Met Gly							
306		250		255		260		
308	gga tct caa aga gtc ctg gag aaa cag tgg acg tgc ttc ctg aag gcg	1050						
309	Gly Ser Gln Arg Val Leu Glu Lys Gln Trp Thr Ser Phe Leu Lys Ala							
310		265		270		275		
312	cgc ttg aac tgc tca gtt cct gga gac tct cat ttt tat ttc aac att	1098						
313	Arg Leu Asn Cys Ser Val Pro Gly Asp Ser His Phe Tyr Phe Asn Ile							
314	280		285		290		295	
316	ctc cag gca gtt aca gat gtg att cgt atc aac ggg cgt gat gtt gtc	1146						
317	Leu Gln Ala Val Thr Asp Val Ile Arg Ile Asn Gly Arg Asp Val Val							
318		300		305		310		
320	ctg gca acg ttt tct aca cct tat aac agc atc cct ggg tct gca gtc	1194						
321	Leu Ala Thr Phe Ser Thr Pro Tyr Asn Ser Ile Pro Gly Ser Ala Val							
322		315		320		325		
324	tgt gcc tat gac atg ctt gac att gcc agt gtt ttt act ggg aga ttc	1242						
325	Cys Ala Tyr Asp Met Leu Asp Ile Ala Ser Val Phe Thr Gly Arg Phe							
326		330		335		340		
328	aag gaa cag aag tct cct gat tcc acc tgg aca cca gtt cct gat gaa	1290						
329	Lys Glu Gln Lys Ser Pro Asp Ser Thr Trp Thr Pro Val Pro Asp Glu							
330		345		350		355		
332	cga gtt cct aag ccc agg cca ggt tgc tgt gct ggc tca tcc tcc tta	1338						
333	Arg Val Pro Lys Pro Arg Pro Gly Cys Cys Ala Gly Ser Ser Ser Leu							
334	360		365		370		375	
336	gaa aga tat gca acc tcc aat gag ttc cct gat gat acc ctg aac ttc	1386						
337	Glu Arg Tyr Ala Thr Ser Asn Glu Phe Pro Asp Asp Thr Leu Asn Phe							
338		380		385		390		
340	atc aag acg cac ccg ctc atg gat gag gca gtg ccc tcc atc ttc aac	1434						
341	Ile Lys Thr His Pro Leu Met Asp Glu Ala Val Pro Ser Ile Phe Asn							
342		395		400		405		

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:5; N Pos. 2882
Seq#:13; N Pos. 22
Seq#:19; N Pos. 1491,1565,1627
Seq#:74; N Pos. 1139,1142,1172
Seq#:76; N Pos. 1143,1146,1176